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1 GCTGTGGGAA CCTCTCCACG CGCAGCAACT CAGCCAAAGG TTTCTGATAG ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCCTC CGAAGGATG  
CGACACCCCTT GGAGAGGTGC GCGTGTCTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT CAAACTGGTC TCTACGTTC CCACCTCCTC CGAAGGATG

101 CGTTAGGGAA CTCTGGGGAC AGAGGGCCCC GCGCCCTGA TGGCCGAGGC AGGGTGGAC CCAGGACCCA GGACGGGTC GGAACCATTA CCATGGCCCC  
GCAATCCCTT GAGACCCCTG TCTGGGGGG GCGGGGACT ACCGGCTCG TCCACGCTG GGTCTGGGT CCGTCCGAG CCCTTGGTAT GGTACCGGGC  
MetalArg

1

201 GATCCCAAG ACCCTAAGT TCGTCTGCT CATCGTCGG GTCCTGCTG CAGTCTTAGC TTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCTCCAG  
CTAGGGCTC TGGGATTCA AGCAGCAGCA GTAGCAGCG GTAGGATCG CAGGACGAG GTACAGACGG AATGAGACGG TGGTGACGG CCGTCTCCT TCAAGGGGTC

4 IleProLys ThrLeuLysP heValValva lileValala valLeuLeup roValleual aTyrSerAla ThrThrAlaA rGlnGluG1 uValProGln

301 CAGACAGTG CCCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGT TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA  
GTCTGTACC GGGGTGCTG TGTCTCCGT TCGAAGTTCC CCTCTCTAC AGGTCTCCT AGATATCTA GTCTGTATG ACCTCGGACA TTGGGCACGT

37 GlnThrVala laProGlnG1 nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACATGAACC TTCTTGCTTC CCATGTACAG TTGTAAATC AGATCAAAAA CATAAAAAGT CCTGCACCAT  
GTCTCCACA CCTAATGTGG TTGCGAAGGT TGTACTTG AAGAACGAG GTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA

71 GluGlyVa lasPtyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrv alcCysLysSe rAspGlnLys HisLysSers erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCGG AAGTGTAGCA GGTGCCCTAG TGGGAAGTGT  
CTGGTCTCTG TGTACACAG TCACATTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCTTCTG

104 ThrArgAsp ThrValCysG lncCysLysG1 uGlyThrPhe ArgAsnGluA snSerProG1 uMetCysArg lysCysSera rGlyGluVal

601 CAAGTCAGTA ATTGTACCTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCGAGC TGCTGAAGAG ACAATGAACA CCAGCCCGG  
GTTCAATCAT TAACATGCAG GACCTACTTA TAGGTACAC AACTCTTAA ACCACGGTTA CCGTGACACC TTGGGGTTCG ACGACTTCTC TGTTACTTGT

137 GlnValserA snCysThrSe rTrpAspAsp ileGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aalaGluGlu ThrMetAsnThr

701 CCAGCCCGG GACTCTCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGG  
GGTCCGGCCC CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGCTCG GGTCCCTGAG GACGGGGTCG ACGACTTCTC TGTTACTGTT GGTCCGGCCC

171 SerProG1 yThrProAla ProAlaAlag luGluThrMe tAsnThrSer ProGlyThrp roAlaProal aalaGluGlu ThrMetThrT hrSerProGly

FIG.- 1A-1

801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG GACTCCTGCC  
CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGGTGGTGG GGGCCCTGAG GACGGGGTGG ACGACTTCTC TGTACTGGT GGTGGGGCCC CTGAGGACGG  
204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl yThrProAla  
901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGT TT GAAAGACTTC ACTGTGGAAG AAATTCTTTC  
AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCTTAGTATC AAGATTAAACA CGAAGACTAA CACAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG  
237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIleVal lleuIleVal ValPheVal  
1001 CTTACCTGAA AGGTTACAGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCCTCC TCTGCTGTGT TCCACAGAC AGAAACGCCT  
GAATGGACTT TCCAGTCCA TCCGGGACCG ACTCCCGCCC CCGCGGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGCTGTCTG TCTTTGCGGA  
1101 GCGCCCTGCC CAAAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA AAAA  
CGGGGACGGG GTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

FIG. 1A-2

1 GCTGTGGGAA CCTCTCCAG CGACGAACT CAGCCAACGA TTTCTGATAG ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCTTAC  
CGACACCCCT GGAGAGGTGC GCGTGTCTGA GTCGTTGCT GTCGTTGCT TAAACCCCT CAAACTGGTC TCTACGTTCC CCACTTCTC GCGAAGGATG  
MetGlnG1 yValLysGlu ArgPheLeuPro  
101 CGTTAGGAA CTCTGGGGAC AGAGCGCCCC GCGCGCTGA TGGCCGAGGC AGGGTGGAC CCAGGACCCA GGACGGCGTC GGAACCATTA CCATGGCCCC  
GCAATCCCTT GAGACCCCTG TCTCGGGGG TCTCGGGGG CCGCGGACT ACCGGCTCG TCCCACGCTG GGTCTGGGT CCTGCCGAG CCTTGGTAT GGTACCGGGC  
-30 LeuGlyAs nserGlyAsp ArgAlaProA rgProProAs pGlyArgGly ArgValArgP roArgThrG1 nAspGlyVal GlyAsnHist hrMetalaArg  
201 GATCCCCAAG ACCCTAAAGT TCGTGTCTGT CATCGTCCGG GTCTGTCTGC CAGTCTTAGC TTAATCTGCC ACCACTGCC GGCAGGAGGA AGTTCCCCAG  
CTAGGGGTTT TGGGATTCA AGCAGCAGCA GTAGCAGCGC CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGG CCGTCTCTCT TCAAGGGGTC  
4 IleProLys ThrLeuLysP heValValva lIleValAla ValLeuLeuP roValLeuAl aTySerAla ThrThrAlaA rgGlnGluG1 uValProGln  
301 CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCGTGCA  
GTCTGTACCC GGGGTGTCTG TGTCTCCGTG TCGAAGTTCC CCGTCTCTAC AGGTCTCTC AGATATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT  
37 GlnThrValA laproGlnG1 nGlnArgHis SerPheLysG lyGluGluCy sproAlaGly serHisArgS erGluHistH rglyAlaCyS AsnProCysThr

FIG. 1B-1

401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTGTAAATC AGATCAAAA CATAAAAGTT CTGCACCAT  
 GTCTCCACA CCTAATGG TTGCGAAGT TGTACTTGG AAGAACGAAG GGTACATGTC AACATTAG TCTAGTTTT GTATTTCAA GGACGTGTA  
 71 GluGlyVa LaspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysse rAspGlnLys HisLysSers erCysThrMet  
 501 GACCAGAGAC ACAGTGTGTC AGTGTAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC  
 CTGGTCTCTG TGTACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTCACATCGT CCACGGGATC ACCCCTTCAG  
 104 ThrArgAsp ThrValCysG lncCysLysG lncCysLysG lncCysLysG lncCysLysG lncCysLysG lncCysLysG lncCysLysG lncCysLysG lncCysLysG  
 601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAAT GCCACTGTGG AAACCCACAG TGCTGAAGAG ACAATGAACA  
 GTTCAGTCAT TAACATGCAG GACCTACTA TAGGTCACAC AACTTCTTAA ACCACGGTTA CCGTGACACC TTGGGGTCCG ACGACTTCTC TGTACTTGT  
 137 GlnValSerA snCysThrse rTrpAspAsp lncGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr  
 701 CCAGCCCGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG  
 GGTCGGGGCC CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGCTGTC GGTCCCTGAG GACGGGGTCC ACGACTTCTC TGTACTGTT TGTACTGTT  
 171 SerProgl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGly  
 801 GACTCCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG GACTCCTGCC  
 CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGCTGTC GGTCCCTGAG GACGGGGTCC ACGACTTCTC TGTACTGTT TGTACTGTT TGTACTGTT  
 204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProgl yThrProAla  
 901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTAATTGT GCTTCTGATT GTGTTTGTTC GAAAGACTTC ACTGTGAAG AAATTCCTTC  
 AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCTAGTATC AAGATTACCA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTAAAGGAAG  
 237 SerSerHigT yrLeuSerCy sThrIleVal GlyIleIleV alLeuIleVal lLeuIleVal ValPheVal  
 1001 CTTACCTGAA AGGTTACGGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCTCTCC TCTGCTGTGT TCCACAGAC AGAAACGCCCT  
 GAATGGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGCCC CCGCGGACCT GTGAGAGACG GGACGGAGGG AGACGACACA AGGGTGTCTG TCTTTGGCGA  
 1101 GCGGACGGG GTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT  
 CCGGACGGG GTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

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FIG. 1B-2

Apo2 1 -----MEQRGQNA<sup>↓</sup>PAASGARKRHGPGPREARGARPGLRVPKTI<sup>↓</sup>VL  
 Apo2DcR 1 -----MARIPKTLKFVV  
 DR4 51 GRGALPTSMGQHGPSARARAGRAPGFRPAREASPRLRVHKTFKFVVVGVL

Apo2 41 VVA<sup>↓</sup>AVLLLVSAESALITQODLAPQORAAPQOKRSSPSEGLCPPGHHISED  
 Apo2DcR 13 VIVAVLLPVLAYSATTARQEEVPOQTVAPQOQRHSFKGEECPAGSHRSEH  
 DR4 101 LQVVPSSAATIK-----LHDQSIGTQQWEHSP<sup>↑</sup>LGELCPPGSHRSEH

Apo2 91 GRDCISCKYQDYSTHWNDLL<sup>CRD1</sup>CLRCTRCDSGEVELSPCTTT<sup>CRD1</sup>RNTVCQCE  
 Apo2DcR 63 TGACN<sup>CRD1</sup>PCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRD<sup>CRD1</sup>IVCQCK  
 DR4 142 FGACNRCTEGVG<sup>CRD1</sup>YTNASN<sup>CRD1</sup>NILFACLPCTACKSDEEERS<sup>CRD1</sup>PCTTT<sup>CRD1</sup>RNTACQCK

Apo2 141 EGTFREEDSP<sup>CRD2</sup>EMCRKCR<sup>CRD2</sup>TGCP<sup>CRD2</sup>GMVKVGDCTP<sup>CRD2</sup>WSDIECVHKE-----  
 Apo2DcR 113 EGTFRNENSP<sup>CRD2</sup>EMCRKCSR-CP<sup>CRD2</sup>SGEVQVSNCTSWDDIQ<sup>CRD2</sup>CV<sup>CRD2</sup>E-EFGANATVE  
 DR4 192 FGTFRNDNSAEMCRK<sup>CRD2</sup>CS<sup>CRD2</sup>TGCP<sup>CRD2</sup>GMVKVKDCTP<sup>CRD2</sup>WSDIECVHKE-----

Apo2 -----  
 Apo2DcR 161 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE  
 DR4 -----

Apo2 183 -----SGIIIGVTVA<sup>CRD3</sup>AVVLI<sup>CRD3</sup>VAVEV-----  
 Apo2DcR 211 ETMTTSPGTPAPAAEETMTTSGTPASSHYLSCTIVGIIIVLIVLLIVFV  
 DR4 234 -----SGNGHNIWVILVVTLVVPLLLVAV-LIVC

Apo2 203 CKSLLWKKVLPYLKGICSGGGGDPERVDRSSQRPGAEDNVLNEIVSILQP  
 DR4 262 CCIGSGCGGDPKCMDRVCFWRLGLIRGPGAEDNAHNEILSNADSLSTFVS

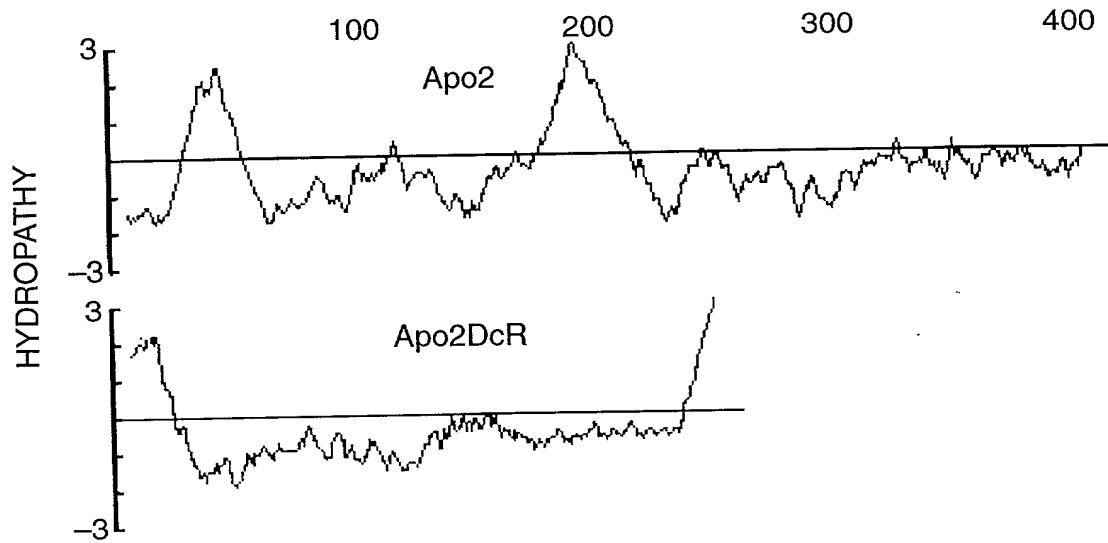
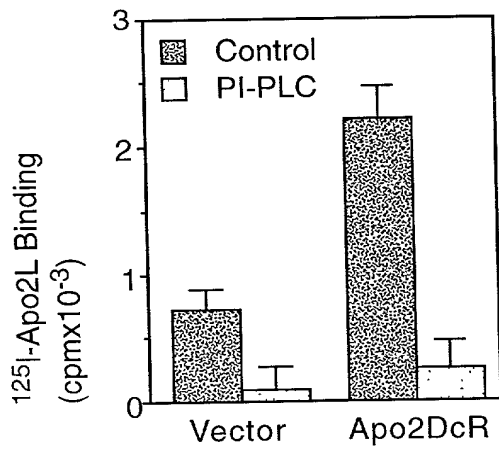
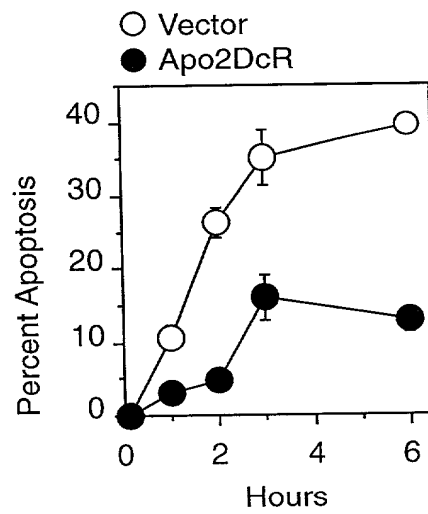
Apo2 253 TQVPEQEMEVOEPAEFTGVNMLSPGESEHLL<sup>CRD4</sup>EPAEAERSQRRRLLVPANE  
 DR4 312 ---EQQMESQEPADLTGVTVQSPGEAQCLLGPAEAEGSQRRRLLVPANG

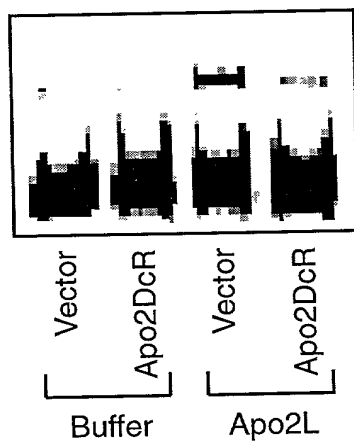
Apo2 303 GDPTETLRQCFDDFADLVPFDSWEPLMRKLG<sup>CRD5</sup>MDNEIKVAKAEAAGH--R  
 DR4 358 ADPTETLMLFEDK<sup>CRD5</sup>FANIVPFDSWDQLMRQLDLTKNEIDVVFRAGTAGP--G  
 Apo3/DR3 338 VMDAVPARRWKEFV<sup>CRD5</sup>RTLGLREAIEAVEVEI-GRF-R  
 TNFR1 322 VVENVPPLRWKEFV<sup>CRD5</sup>RRGLSDHEIDRIELQN-GRCLR  
 CD95 220 IAGVHTLSQVKGFVRKNGVNEAKIDEIKNDN-VQDTA

Apo2 351 D<sup>\*</sup>ILY<sup>\*</sup>TMLIKWV<sup>\*</sup>NKTGR-DASVHTLLDALETIGERLAKOKIEDHLLSSGKF  
 DR4 406 DALYAMLK<sup>\*</sup>WV<sup>\*</sup>NKTGR-NASHTLLDALERM<sup>\*</sup>EEERHAK<sup>\*</sup>EKI<sup>\*</sup>QDLLVDSGKF  
 Apo3/DR3 374 DQQYEMLK<sup>\*</sup>RW<sup>\*</sup>RQQP---AGLGAVYAALERMGLDGCVEDLRS  
 TNFR1 358 EAQYSMLATWRRRT<sup>\*</sup>ERREATLEILGRVLRDMDLIGCLEDIEE  
 CD95 256 EQKVQILLRNWHQLHGKKEAY-DTLIKDLK<sup>\*</sup>KANLCTLAERIQ<sup>\*</sup>T

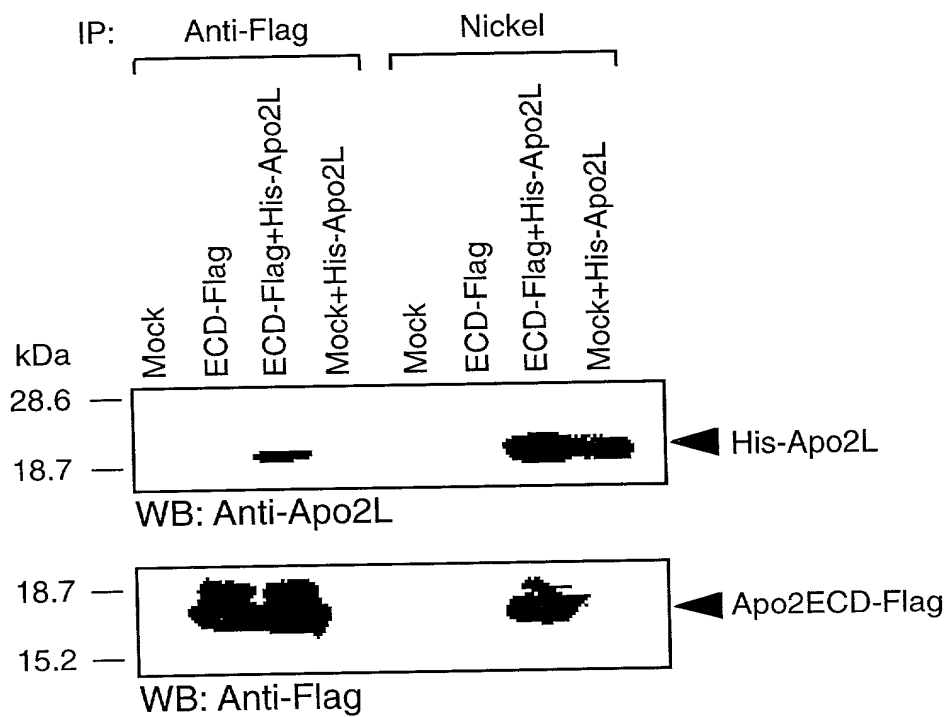
Apo2 400 MYLEGNADSALS  
 DR4 455 IYLEDGTGSAVSLE

FIG.\_2

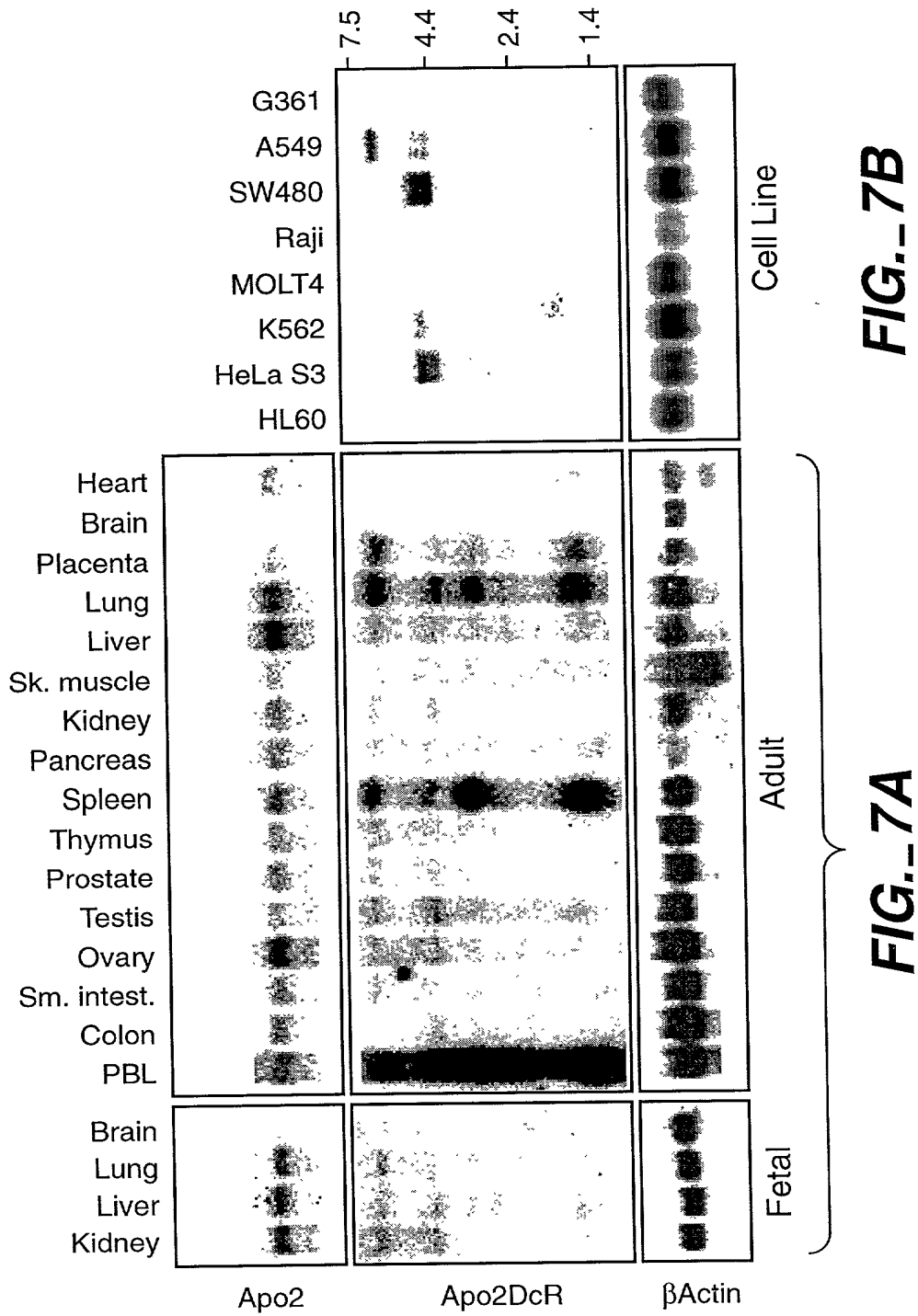
**FIG.\_3****FIG.\_4****FIG.\_5**



**FIG.\_6**



**FIG.\_10**



1	CCCACGGCGTC	CGCATAAATC	AGACAGCGGGC	CGGAGAAACC	CGCAATCTCT	CGGCCACAA	AATACACCGA	CGATGCCCGA	TCTACTTTAA	GGCGTGAAC
	GGGTGGCAG	GCGTATTTAG	TGGTGGCG	GCTCTTTGG	GCGTTAGAG	GCGGGTGTT	TTATGTGGCT	GCTACGGGCT	AGATGAAATT	CCGACCTTG
101	CCACGGGCGCT	GAGAGACTAT	AAGACGGTTC	CCTACCGCCA	TGGAACACG	GGGACAGAAC	GCCCCGGCG	CTTCGGGGC	CCGAAAAAGG	CACGGGCCAG
	GGTGCCCGGA	CTCTCTGATA	TTCTGCAAG	GGATGGCGGT	ACCTTGTTGC	CCCTGTCTTG	CGGGGGCGG	GAAGCCCCG	GGCTTTTCC	GTGCGGGTC
1				M	etGluGlnAr	gGlyGlnAsn	AlaProAla	laSerGlyAl	aArgLysArg	HisGlyProGly
201	GACCCAGGGA	GGCCGGGGG	GCCAGGCCTG	GGCTCCGGGT	CCCCAAGACC	CTTGTGCTCG	TTGTGCGCG	GGTCTGCTG	TTGGTCTCAG	CTCAGTCTGC
	CTGGTCCCT	CCGCGCCCT	CGTCCGGAC	CCGAGGCCCA	GGGTCTCTG	GAACACGAGC	AACAGCGGG	CCAGCAGAC	AACACAGATC	GACTCAGACG
22	ProArgG1	uAlaArgGly	AlaArgProG	lyLeuArgVa	lProLysThr	LeuValLeuV	alValAlaAl	aValLeuLeu	LeuValSerA	laGluSerAla
301	TCTGATCACC	CAACAAGACC	TAGCTCCCA	GCAGAGAGCG	GGCCCAACAC	AAAAGAGGTC	CAGCCCCCTCA	GAGGATTGT	GTCCACCCTGG	ACACCATATC
	AGACTAGTGG	GTGTCTCTGG	ATCAGGGGT	CGTCTCTCG	CGGGGTGTTG	TTTTCTCCAG	GTCCGGGAGT	CTCCCTAAC	CAGGTGGACC	TGTGGTATAG
55	LeulleThr	GlnGlnAspL	euAlaProG1	nglnArgAla	AlaProGlnG	lnLysArgSe	rSerProSer	GluGlyLeuC	ysProProG1	yHisHisIle
401	TCAGAAGACG	GTAGAGATTG	CATCTCTCTG	AAATATGGAC	AGGACTATAG	CACTCACTGG	AATGACCTCC	TTTTCTGCTT	CGGCTGCACC	AGGTGTGATT
	AGTCTTCTGC	CATCTCTAAC	GTAGAGACG	TTTATACCTG	TCCTGATATC	GTGAGTGACC	TTACTGGAGG	AAAAGACGAA	CGGACCGTGG	TCCACACTAA
88	SerGluAspG	lyArgAspCy	sIleSerCys	LysTyrGlyG	lnAspTyrse	rThrHisTrp	AsnAspLeuL	euPheCysLe	uArgCysThr	ArgCysAspser
501	CAGGTGAAGT	GGAGCTAAGT	CCCTGCACCA	CGACCAGAAA	CACAGTGTGT	CAGTGGGAAG	AAGGCACCTT	CCGGGAAGAA	GATTCTCCTG	AGATGTGCCG
	GTCCACTTCA	CCTCGATTCA	GGGACGTGGT	GCTGGTCTTT	GTGTCACACA	GTACCGCTTC	TTCCGTGGAA	GGCCTTCTT	CTAAGAGGAC	TCTACACGGC
122	GlyGluVa	lGluLeuser	ProCysThrT	hrThrArgAs	nThrValCys	GlnCysGluG	luGlyThrPh	eArgGluGlu	AspserProG	luMetCysArg
601	GAAGTGCCCG	ACAGGGGTGC	CCAGAGGGAT	GGTCAAGGTC	GGTGATTGTA	CACCTGGAG	TGACATCGAA	TGTGTCCACA	AAGAATCAGG	CATCATCAT
	CTTCACGGCG	TGTCCACAG	GGTCTCCCTA	CCAGTTCAC	CCACTAACAT	GTGGGACCTC	ACTGTAGCTT	ACACAGGTGT	TTCTTAGTCC	GTAGTAGTAT
155	LysCysArg	ThrGlyCysP	roArgGlyMe	tValLysVal	GlyAspCyst	hrProTrpse	rAspIleGlu	CysValHisL	ysGluSerG1	yIleIleIle
701	GGAGTCACAG	TTGCAGCCGT	AGTCTTGATT	GTGGCTGTGT	TTGTTTGCAA	GTCTTTACTG	TGGAAGAAAG	TCCTTCCTTA	CCTGAAAGGC	ATCTGCTCAG
	CCTCAGTGTG	AACGTGGCA	TCAGAACTAA	CACCGACACA	AACAAACGTT	CAGAAATGAC	ACCTTCTTTC	AGGAGGAAT	GGACTTTCCG	TAGACGAGTC
188	GlyValThrV	alAlaAlaVa	lValLeuIle	ValAlaValP	heValCysLy	sSerLeuLeu	TrpLysLysV	alleuProTy	rLeuLysGly	IleCysSerGly

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801 GTGCTGGTGG GGACCCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCCTCAA TGAGATCGTG AGTATCTTGC AGCCACCCCA  
 CACCACCACC CCTGGGACTC GCACACCCTGT CTTGAGTGT TGTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT  
 222 GlyGlyG1 yAspProGlu ArgValAspA rgSerSerG1 nArgProGly AlaGluAspA snValLeuAs nGluLeVal SerIleLeuG InProThrGln  
 901 GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA  
 CCAGGGACTC GTCCTTTACC TTCAGGTCCT CCGTCGTCTC GGTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT  
 255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alaSnMetLe uSerProGly GluSerGluH isLeuLeuG1 uProAlaGlu  
 1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCCTTGA TGACTTTGCA GACTTGGTGC  
 CGACTTTCCA GAGTCTCCTC CTCGAGCAGC CAAGGTCGTT TACTTCCACT AGGTGACTC TGAGACTCTG TCACGAGGCT ACTGAAACGT CTGAACCACG  
 288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG InCysPheAs pAspPheAla AspLeuValPro

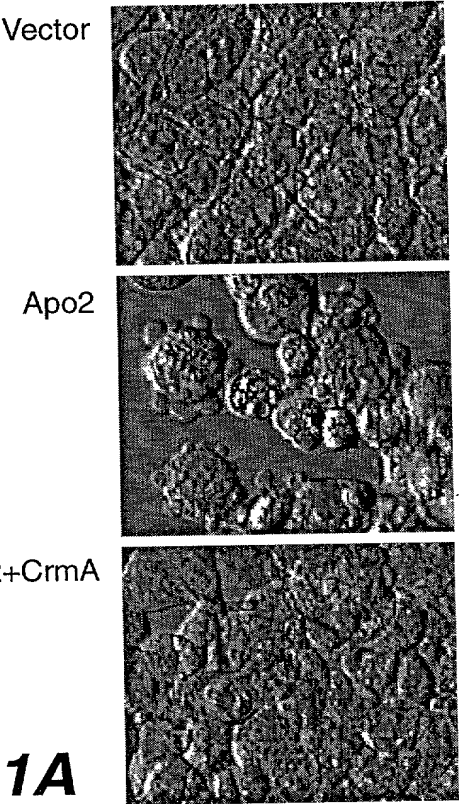
FIG.-8A-2

1101 CCTTTGACTC CTGGGAGCCG CTCATGACGA AGTTGGGCCT CATGGACAAT GAGATAAAGG TGGCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA  
 GGAACACTGAG GACCTCGGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCATTTCC ACCGATTTCG ACTCCGTCCG CCGGTGTCCC TGCGAACAT  
 322 PheAspSe rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysV alalaLysAl aGluAlaAla GlyHisArgA spThrLeuTyr  
 1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCTGTCT GATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG  
 GTGCTACGAC TATTTCACCC AGTTGTTTTG GCGGCTCTA CCGAGACAGG TGTGGGACGA CCTACGGAAAC CTCCTCGACC CTCCTCTCTGA ACGGTTCTGTC  
 355 ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaSerValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln  
 1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA  
 TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAAAC GGATTCACAC TAAGAGAAGT CCTTCACTCT  
 388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXqqS erOC\*  
 1401 CCTTCCCCTG TTTACCTTTT TTCTGGAANA AGCCCAACTG GACTCCAGTC AGTAGGAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC  
 GGAAGGACC AAATGGAAA AAGACCTTTT TCGGGTTGAC CTGAGGTGAC TCATCCTTTC ACGGTGTTAA CAGTGTA CTG GCAATGACCT TCTTTGAGAG  
 1501 CCATCCAAAC TCACCCAGTG GATGGAACAT CCTGTAACCT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAT  
 GGTAGGTTGT AGTGGTCCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTTCG ACTTACACTA TTATTCTCTGT GATACCTTTA  
 1601 GTCTGGATCA TTCCGTTTGT GCGTACTTGT AGATTGGTTT TGGGATGTCA TTGTTTTCAC AGCACTTTT TATCCTAATG TAAATGCTTT ATTTATTAT  
 CAGACCTAGT AAGGCAACA CCCATGAAC TCTAAACCA ACCCTACAGT AACAAAAGTG TCGTGAANA ATAGGATTAC ATTTACGAAA TAAATAAATA  
 1701 TTGGGCTACA TTGTAAGATC CATCTACAA AAAAAAAG GCGGCGCGC ACTCTAGACT CGACCTGCAG AAGCTTGGCC GCCATGGCC  
 AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTT CCGCGGCGC TGACATCTCA GCTGGACGTC TTCGAACCGG CGGTACCGG

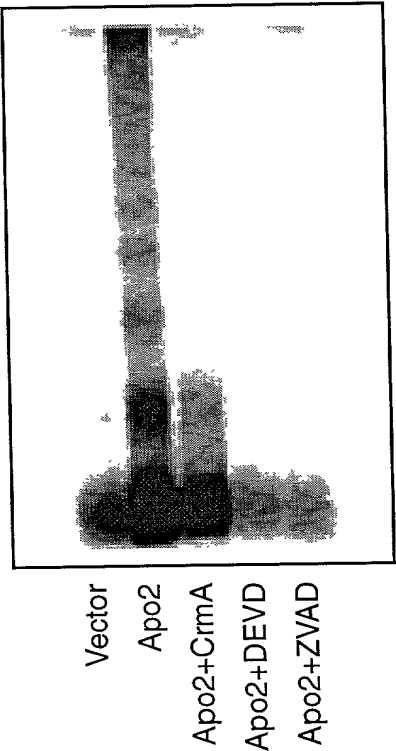
FIG.-8B

1 MEORGONAPAASGARKRHGPGPREARGARGLRVPKTLVLVAAVLLLVSAESALITQQD  
 61 LAPOQRAAPQOKRSPSEGLCPPGHHISEDGRDCISCKYQDYSTHWNDLFLCRLCTRCD  
 121 SGEVELSPCTTTRNTVQCCEGTFREEDSPEMCRKCRGTGCPGMVKVGDCTPWSDIQVH  
 181 KESGIIIGVTVAAVLIVAVFVCKSLWKVLPYLKIGCSGGGDPVDRSSQRPGEAED  
 241 NVLNEIVSILQPTQVPEQEMEVEQEPAEPTGVNMLSPGESEHLLLEPAEAERSQRRRLVPA  
 301 NEGDPTETRLQCDFDDFADLVPFDSWEPLMRKLGMDNEIKVAKAEAGHRDTLYTMLIKW  
 361 VNKTGRDASVHTLLDALETJGERLAKQKIEDHLLSSGKFMYLEGNADSALS

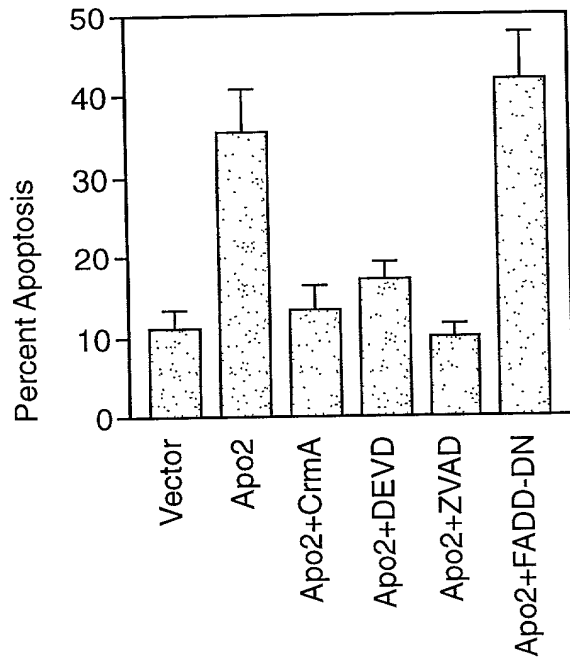
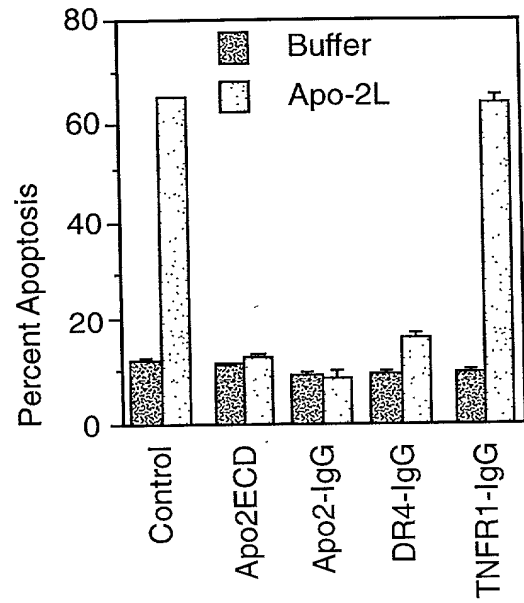
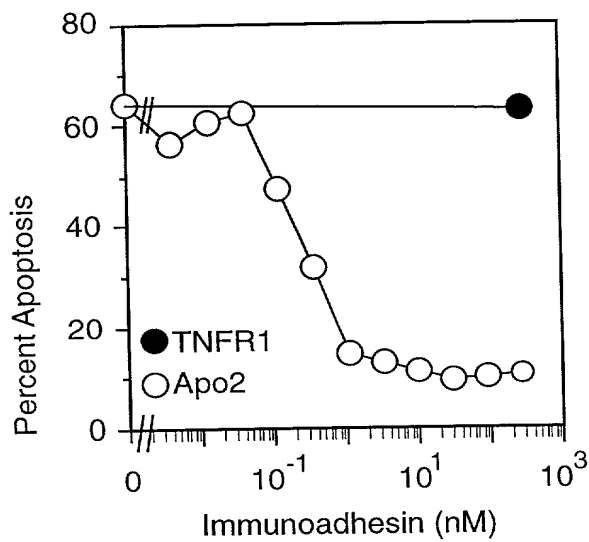
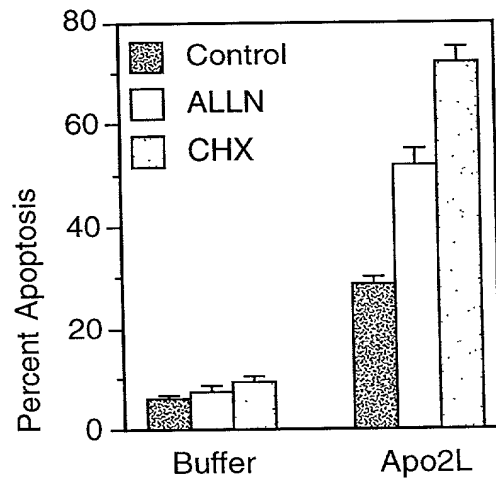
FIG.-9



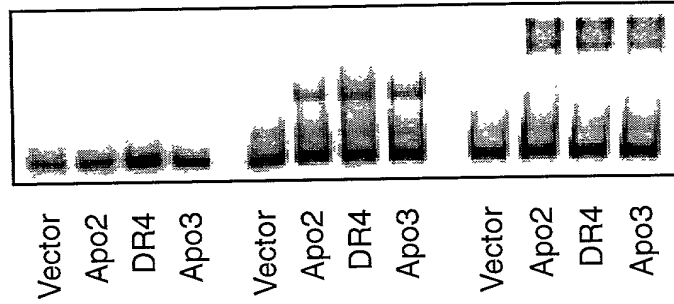
**FIG.\_11A**



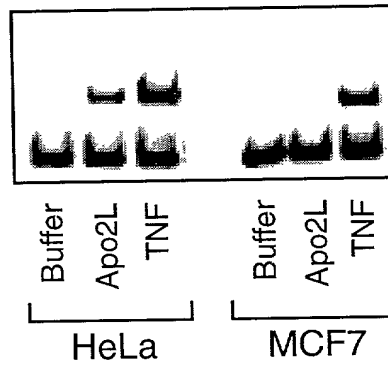
**FIG.\_11B**

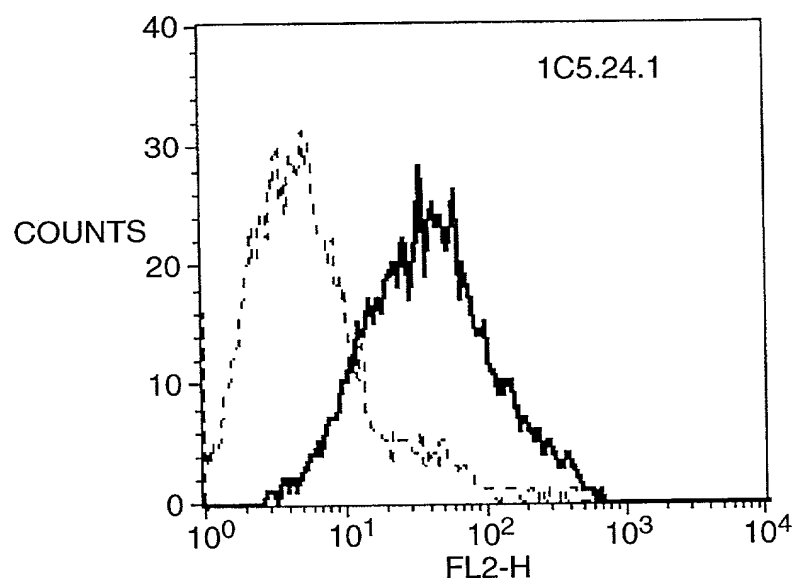
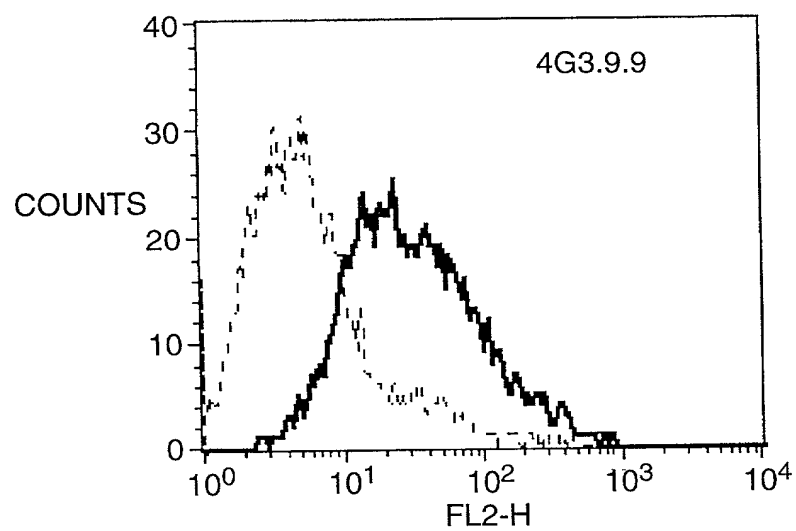
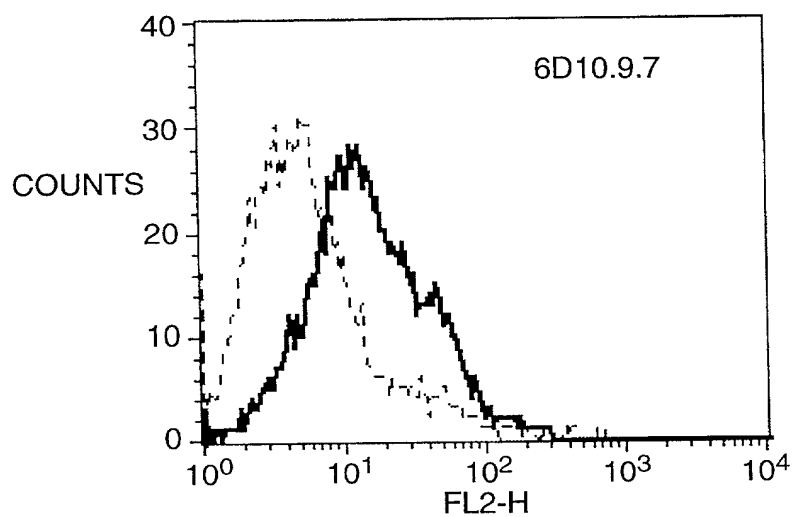
**FIG. 11C****FIG. 11D****FIG. 11E****FIG. 12C**

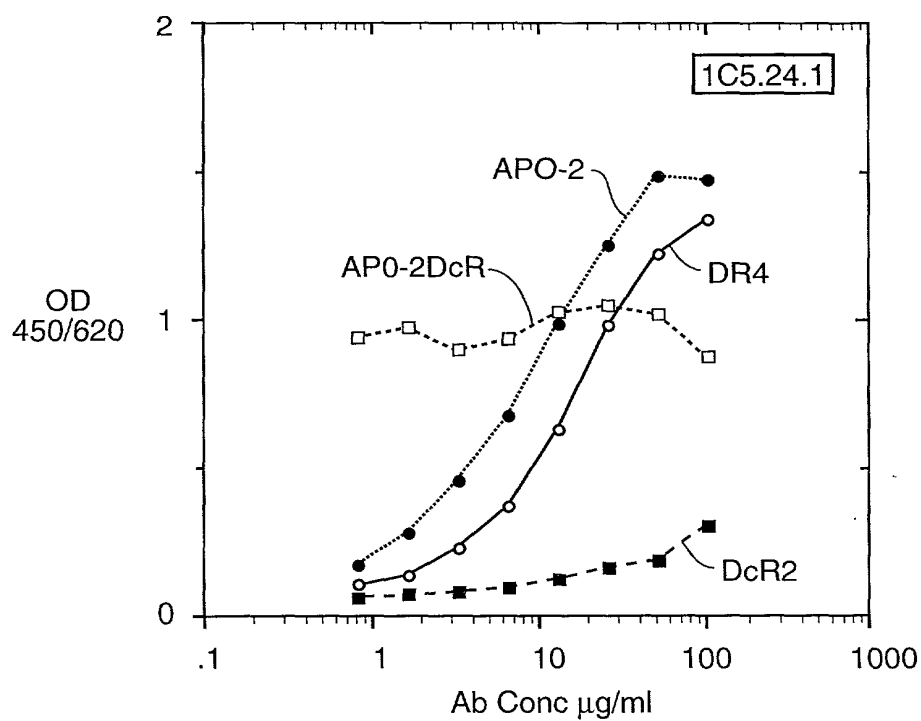
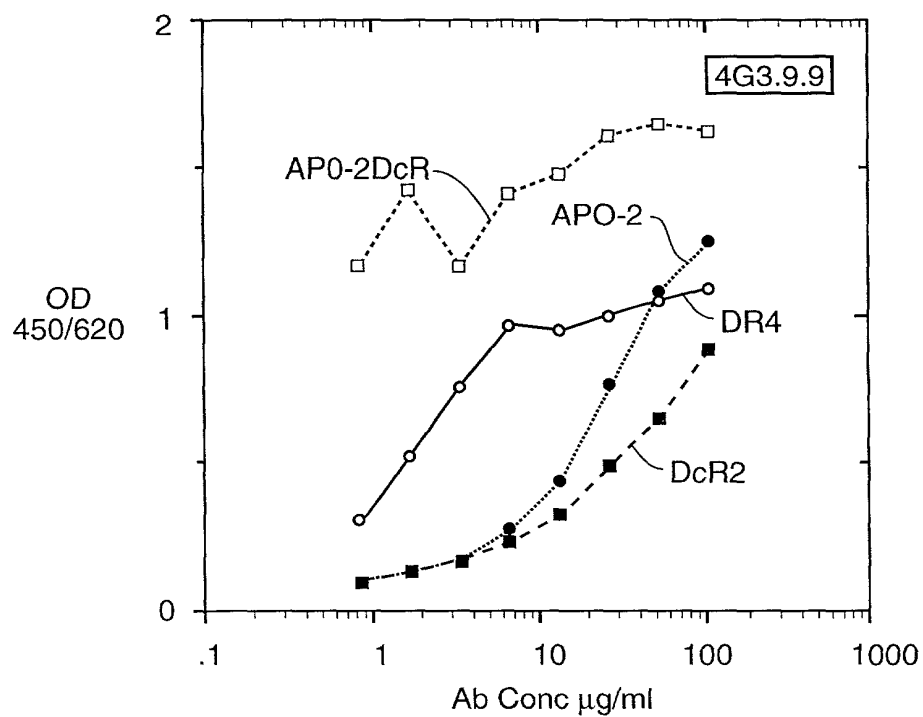
Unlabelled probe	+	+	+	+	-	-	-	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+	+	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-	-	-	+	+	+	+	+

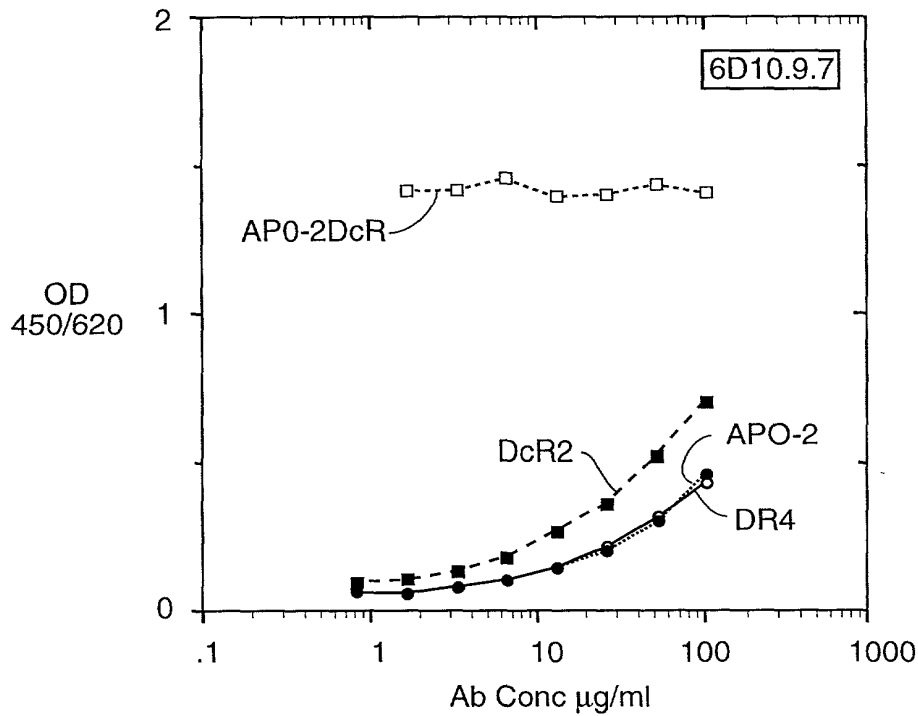
**FIG.\_12A**

Unlabelled probe	-	-	-	-	-	-
Labelled probe	+	+	+	+	+	+
Anti-p65	-	-	-	-	-	-

**FIG.\_12B****FIG.\_13**

**FIG.\_14A****FIG.\_14B****FIG.\_14C**

**FIG. 15A****FIG. 15B**

**FIG. 15C**

## Summary of mAbs to DcR1

mAbs	ISOTYPE	FACS (HUMEC)	Cross reactivity			
			DR4	Apo-2	Apo-2DcR	DcR2
1C5.24.1	IgG1	+	++	+++	+++	-
4G3.9.9	IgG1	+	++	+	+++	+/-
6D10.9.7	IgG2b	+	-	-	+++	+/-

Percent Cross reactivity was determined by comparing the binding capacity to Apo-2DcR at 10 ug/ml of mAbs in ELISA. ++: >75% , +: 25-75%, +/-:10-25%, -: <10% .

**FIG. 16**